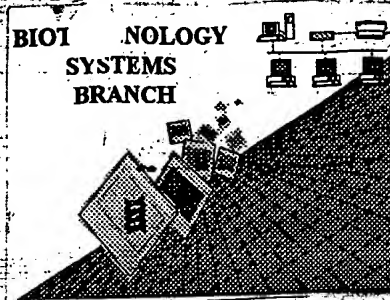# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/674,237_

Source: _PCT/09_

Date Processed by STIC: _1/11/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>   <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _09/674,237_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)   Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)   Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

PCT09

RAW SEQUENCE LISTING   DATE: 01/11/2001
PATENT APPLICATION: US/09/674,237   TIME: 17:14:19

Input Set : A:\Egan1.app
Output Set: N:\CRF3\01112001\I674237.raw

Does Not Comply
Corrected Diskette Needed

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   5 <120> TITLE OF INVENTION: ESE GENES AND PROTEINS
   7 <130> FILE REFERENCE: 3206-169/PAR
   9 <140> CURRENT APPLICATION NUMBER: US/09/674,237
  10 <141> CURRENT FILING DATE: 2000-10-27
  12 <150> PRIOR APPLICATION NUMBER: 2,230,201
  13 <151> PRIOR FILING DATE: 1998-04-27
  15 <160> NUMBER OF SEQ ID NOS: 33
  17 <170> SOFTWARE: PatentIn Ver. 2.0
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OK

ERRORED SEQUENCES

p.4

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 513 <211> LENGTH: 1213
 514 <212> TYPE: PRT
 515 <213> ORGANISM: Mus musculus
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 521 Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe Leu Ser Leu
 522              20                  25                  30
 524 Lys Pro Ile Ala Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe
 525          35                  40                  45
 527 Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu
 528      50                  55                  60
 530 Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile
 531  65                  70                  75                  80
 533 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Gln Leu Pro Ser
 534              85                  90                  95
 536 Thr Leu Pro Pro Val Met Lys Gln Gln Pro Val Ala Ile Ser Ser Ala
 537             100                 105                 110
 539 Pro Ala Phe Gly Ile Gly Gly Ile Ala Ser Met Pro Pro Leu Thr Ala
 540             115                 120                 125
 542 Val Ala Pro Val Pro Met Gly Ser Ile Pro Val Val Gly Met Ser Pro
 543         130                 135                 140
 545 Pro Leu Val Ser Ser Val Pro Pro Ala Ala Val Pro Pro Leu Ala Asn
 546 145                 150                 155                 160
 548 Gly Ala Pro Pro Val Ile Gln Pro Leu Pro Ala Phe Ala His Pro Ala
 549             165                 170                 175
 551 Ala Thr Trp Pro Lys Ser Ser Ser Phe Ser Arg Ser Gly Pro Gly Ser
 552             180                 185                 190
 554 Gln Leu Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Ala Ser
 555         195                 200                 205
 557 Ala Pro Pro Ala Ala Glu Trp Ala Val Pro Gln Ser Ser Arg Leu Lys
 558         210                 215                 220
 560 Tyr Arg Gln Leu Phe Asn Ser His Asp Lys Thr Met Ser Gly His Leu
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561 225                     230                     235                     240
563 Thr Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln
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566 Ala Gln Leu Ala Ser Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly
567                 260                     265                     270
569 Lys Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val
570                 275                     280                     285
572 Ala Met Ser Gly Gln Pro Leu Pro Pro Val Leu Pro Pro Glu Tyr Ile
573             290                     295                     300
575 Pro Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Met Ser Val Ile
576 305                     310                     315                     320
578 Ser Ser Ser Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Ser Ser Glu
579                 325                     330                     335
581 Asp Glu Gln Gln Pro Glu Lys Lys Leu Pro Val Thr Phe Glu Asp Lys
582             340                     345                     350
584 Lys Arg Glu Asn Phe Glu Arg Gly Ser Val Glu Leu Glu Lys Arg Arg
585             355                     360                     365
587 Gln Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala Gln
588         370                     375                     380
590 Leu Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Glu Gln
591 385                     390                     395                     400
593 Glu Ala Lys Arg Gln Leu Glu Leu Glu Lys Gln Leu Glu Lys Gln Arg
594                 405                     410                     415
596 Glu Leu Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg
597             420                     425                     430
599 Arg Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu Trp
600         435                     440                     445
602 Glu Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Lys Glu Gln
603     450                     455                     460
605 Glu Gly Thr Val Val Leu Lys Ala Arg Arg Lys Thr Leu Glu Phe Glu
606 465                     470                     475                     480
608 Leu Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu Gln
609             485                     490                     495
611 Asp Ile Arg Cys Arg Leu Ala Thr Gln Arg Gln Glu Ile Glu Ser Thr
612             500                     505                     510
614 Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln
615         515                     520                     525
617 Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu Lys
618     530                     535                     540
620 Gln Ile Leu Ser Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His
621 545                     550                     555                     560
623 Arg Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu Leu
624                 565                     570                     575
626 Ala Arg Gln Gln Leu Arg Glu Gln Leu Asp Glu Val Glu Arg Glu Thr
627             580                     585                     590
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630         595                     600                     605
632 Leu Arg Glu Ile His Ser Lys Gln Gln Leu Gln Lys Gln Arg Ser Leu
633     610                     615                     620
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639             645             650             655
641 Lys Gln Trp Leu Glu His Val Gln Gln Glu Glu Gln Pro Arg Pro Arg
642             660     .       665             670
644 Lys Pro His Glu Glu Asp Arg Leu Lys Arg Glu Asp Ser Val Arg Lys
645         675             680             685
647 Lys Glu Ala Glu Glu Arg Ala Lys Pro Glu Met Gln Asp Lys Gln Ser
648     690             695             700
650 Arg Leu Phe His Pro His Gln Glu Pro Ala Lys Leu Ala Thr Gln Ala
651 705             710             715             720
653 Pro Trp Ser Thr Thr Glu Lys Gly Pro Leu Thr Ile Ser Ala Gln Glu
654             725             730             735
656 Ser Val Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu Ser Arg
657             740             745             750
659 Ser His Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met Val Asp
660     755             760             765
662 Glu Ser Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly
663     770             775             780
665 Lys Thr Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile Pro Glu Asn
666 785             790             795             800
668 Glu Val Pro Thr Pro Ala Lys Pro Val Thr Asp Leu Thr Ser Ala Pro
669             805             810     .       815
671 Ala Pro Lys Leu Ala Leu Arg Glu Thr Pro Ala Pro Leu Pro Val Thr
672             820             825             830
674 Ser Ser Glu Pro Ser Thr Thr Pro Asn Asn Trp Ala Asp Phe Ser Ser
675             835             840             845
677 Thr Trp Pro Ser Ser Ser Asn Glu Lys Pro Glu Thr Asp Asn Trp Asp
678     850             855             860
680 Thr Trp Ala Ala Gln Pro Ser Leu Thr Val Pro Ser Ala Gly Gln Leu
681 865             870             875             880
683 Arg Gln Arg Ser Ala Phe Thr Pro Ala Thr Ala Thr Gly Ser Ser Pro
684             885             890             895
686 Ser Pro Val Leu Gly Gln Gly Glu Lys Val Glu Gly Leu Gln Ala Gln
687             900             905             910
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690             915             920             925
692 Lys Ser Asp Val Ile Thr Val Leu Glu Gln Gln Asp Met Trp Trp Phe
693     930             935             940
695 Gly Glu Val Gln Gly Gln Lys Gly Trp Phe Pro Lys Ser Tyr Val Lys
696 945             950             955             960
698 Leu Ile Ser Gly Pro Val Arg Lys Ser Thr Ser Ile Asp Thr Gly Pro
699             965     .       970             975
701 Thr Glu Ser Pro Ala Ser Leu Lys Arg Val Ala Ser Pro Ala Ala Lys
702             980             985             990
704 Pro Ala Ile Pro Gly Glu Glu Phe Ile Ala Met Tyr Thr Tyr Glu Ser
705         995             1000            1005
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RAW SEQUENCE LISTING   DATE: 01/11/2001
PATENT APPLICATION: US/09/674,237   TIME: 17:14:19

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Output Set: N:\CRF3\01112001\I674237.raw

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       714 .           1045                1050                1055
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       717         1060                1065                1070
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       720     1075                1080                1085
       722 Ala Pro Gly Gln Leu Ile Leu Ile Arg Lys Lys Asn Pro Gly Gly Trp
       723    1090                1095                1100
       725 Trp Glu Gly Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Ile Gly Trp
E-->   726(105)           1110                1115                1120
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       732         1140                1145                1150
       734 Val Ile Gly Met Tyr Asp Tyr Thr Ala Gln Asn Asp Asp Glu Leu Ala
       735    1155                1160                1165
       737 Phe Ser Lys Gly Gln Ile Ile Asn Val Leu Asn Lys Glu Asp Pro Asp
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      1234 Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Thr Phe Phe
      1235            35              40              45
      1237 Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu
      1238         50              55              60
      1240 Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile
      1241   65          '       70              75              80
      1243 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro Val
      1244               85              90              95
      1246 Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile
      1247            100             105             110
      1249 Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln
      1250         115             120             125
      1252 Pro Leu Pro Pro Val Ala Pro Ile Ala Thr Pro Leu Ser Ser Ala Thr
      1253    130             135             140
      1255 Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro
```

p.7

When numbering first amino acid on a line, begin the number under the first letter of the amino acid. Please leave a space between entire number and next amino acid.

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1256 145                    150                   155                    160
1258 Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln
1259                   165                   170                    175
1261 Pro Leu Ser Ile Pro Tyr Ser Ser Ser Thr Leu Pro His Ala Ser Ser
1262              180                   185                   190
1264 Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala
1265   195                   200                   205
1267 Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Ser Thr Ser Ser Thr Ala
1268      210                   215                   220
1270 Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val
1271 225                   230                   235                    240
1273 Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp
1274              245                   250                   255
1276 Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu
1277              260                   265                   270
1279 Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu
1280      275                   280                   285
1282 Ala Asp Ile Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu
1283      290                   295                   300
1285 Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu
1286 305                   310                   315                    320
1288 Thr Leu Pro Pro Glu Leu Val Pro Pro Ser Phe Arg Gly Gly Lys Gln
1289              325                   330                   335
1291 Val Asp Ser Val Asn Gly Thr Leu Pro Ser Tyr Gln Lys Thr Gln Glu
1292      340                   345                   350
1294 Glu Glu Pro Gln Lys Lys Leu Pro Val Thr Phe Glu Asp Lys Arg Lys
1295      355                   360                   365
1297 Ala Asn Tyr Glu Arg Gly Asn Met Glu Leu Glu Lys Arg Arg Gln Val
1298      370                   375                   380
1300 Leu Met Glu Gln Gln Gln Arg Glu Ala Glu Arg Lys Ala Gln Lys Glu
1301 385                   390                   395                    400
1303 Lys Glu Glu Trp Glu Arg Lys Gln Arg Glu Leu Gln Glu Gln Glu Trp
1304              405                   410                   415
1306 Lys Lys Gln Leu Glu Leu Glu Lys Arg Leu Glu Lys Gln Arg Glu Leu
1307      420                   425                   430
1309 Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg Arg Glu
1310      435                   440                   445
1312 Ala Ala Lys Gln Glu Leu Glu Arg Gln Arg Arg Leu Glu Trp Glu Arg
1313      450                   455                   460
1315 Leu Arg Arg Gln Glu Leu Leu Ser Gln Lys Thr Arg Glu Gln Glu Asp
1316 465                   470                   475                    480
1318 Ile Val Arg Leu Ser Ser Arg Lys Lys Ser Leu His Leu Glu Leu Glu
1319              485                   490                   495
1321 Ala Val Asn Gly Lys His Gln Gln Ile Ser Gly Arg Leu Gln Asp Val
1322              500                   505                   510
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1328      530                   535                   540
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1339 Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser
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1358      690                  695                  700
1360 Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val
1361 705                  710                  715                  720
1363 Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met
1364              725                  730                  735
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1367              740                  745                  750
1369 Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe
1370          755                  760                  765
1372 Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser
1373      770                  775                  780
1375 Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser
1376 785                  790                  795                  800
1378 Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser
1379              805                  810                  815
1381 Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe
1382          820                  825                  830
1384 Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly
1385          835                  840                  845
1387 Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala
1388      850                  855                  860
1390 Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val
1391 865                  870                  875                  880
1393 Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg
1394              885                  890                  895
1396 Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val
1397          900                  905                  910
1399 Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro
1400      915                  920                  925
1402 Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,237

DATE: 01/11/2001
TIME: 17:14:19

Input Set : A:\Egan1.app
Output Set: N:\CRF3\01112001\I674237.raw

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1408 Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu
1409                    965                   970              975
1411 Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn
1412           980                   985              990
1414 Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser
1415      995              1000                  1005
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1418      1010                  1015                  1020
1420 Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln Leu Ile
E-->  1422 025                  1030                  1035              1040
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1424                  1045                  1050                  1055
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1427           1060                   1065                  1070
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1430      1075                  1080                  1085
1432 Val Cys Gln Val Ile Ala Met Tyr Asp Tyr Met Ala Asn Asn Glu Asp
1433      1090                  1095                  1100
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E-->  1436 105                  1110                  1115              1120
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1439                  1125                  1130                  1135
1441 Pro Ser Asn Tyr Val Lys Met Thr Thr Asp Ser Asp Pro Ser Gln Gln
1442           1140                   1145                  1150
1444 Trp Cys Ala Asp Leu Gln Ala Leu Asp Thr Met Gln Pro Thr Glu Arg
1445      1155                  1160                  1165
1447 Lys Arg Gln Gly Tyr Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr
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2760           20                  25                  30
2762 Lys Pro Ile Ala Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe
2763           35                  40                  45
2765 Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu
2766      50                  55                  60
2768 Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile
2769 65                  70                  75              80
2771 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Gln Leu Pro Ser
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same error

pp 10-12

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2772                      85                    90                    95
2774 Thr Leu Pro Pro Val Met Lys Gln Gln Pro Val Ala Ile Ser Ser Ala
2775                     100                   105                   110
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2778                115                   120                   125
2780 Val Ala Pro Val Pro Met Gly Ser Ile Pro Val Val Gly Met Ser Pro
2781      130                   135                   140
2783 Pro Leu Val Ser Ser Val Pro Pro Ala Ala Val Pro Pro Leu Ala Asn
2784 145                   150                   155                   160
2786 Gly Ala Pro Pro Val Ile Gln Pro Leu Pro Ala Phe Ala His Pro Ala
2787                165                   170                   175
2789 Ala Thr Trp Pro Lys Ser Ser Ser Phe Ser Arg Ser Gly Pro Gly Ser
2790                180                   185                   190
2792 Gln Leu Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Ala Ser
2793                195                   200                   205
2795 Ala Pro Pro Ala Ala Glu Trp Ala Val Pro Gln Ser Ser Arg Leu Lys
2796      210                   215                   220
2798 Tyr Arg Gln Leu Phe Asn Ser His Asp Lys Thr Met Ser Gly His Leu
2799 225                   230                   235                   240
2801 Thr Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln
2802                245                   250                   255
2804 Ala Gln Leu Ala Ser Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly
2805                260                   265                   270
2807 Lys Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val
2808                275                   280                   285
2810 Ala Met Ser Gly Gln Pro Leu Pro Pro Val Leu Pro Pro Glu Tyr Ile
2811      290                   295                   300
2813 Pro Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Met Ser Val Ile
2814 305                   310                   315                   320
2816 Ser Ser Ser Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Ser Ser Glu
2817                325                   330                   335
2819 Asp Glu Gln Gln Pro Glu Lys Lys Leu Pro Val Thr Phe Glu Asp Lys
2820                340                   345                   350
2822 Lys Arg Glu Asn Phe Glu Arg Gly Ser Val Glu Leu Glu Lys Arg Arg
2823                355                   360                   365
2825 Gln Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala Gln
2826      370                   375                   380
2828 Leu Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Glu Gln
2829 385                   390                   395                   400
2831 Glu Ala Lys Arg Gln Leu Glu Leu Glu Lys Gln Leu Glu Lys Gln Arg
2832                405                   410                   415
2834 Glu Leu Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg
2835                420                   425                   430
2837 Arg Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu Trp
2838                435                   440                   445
2840 Glu Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Lys Glu Gln
2841      450                   455                   460
2843 Glu Gly Thr Val Val Leu Lys Ala Arg Arg Lys Thr Leu Glu Phe Glu
2844 465                   470                   475                   480
```

```
2846 Leu Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu Gln
2847                 485                 490                 495
2849 Asp Ile Arg Cys Arg Leu Ala Thr Gln Arg Gln Glu Ile Glu Ser Thr
2850             500                 505                 510
2852 Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln
2853         515                 520                 525
2855 Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu Lys
2856     530                 535                 540
2858 Gln Ile Leu Ser Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His
2859 545                 550                 555                 560
2861 Arg Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu Leu
2862                 565                 570                 575
2864 Ala Arg Gln Gln Leu Arg Glu Gln Leu Asp Glu Val Glu Arg Glu Thr
2865             580                 585                 590
2867 Arg Ser Lys Leu Gln Glu Ile Asp Val Phe Asn Asn Gln Leu Lys Glu
2868         595                 600                 605
2870 Leu Arg Glu Ile His Ser Lys Gln Gln Leu Gln Lys Gln Arg Ser Leu
2871     610                 615                 620
2873 Glu Ala Ala Arg Leu Lys Gln Lys Glu Gln Glu Arg Lys Ser Leu Glu
2874 625                 630                 635                 640
2876 Leu Glu Lys Gln Lys Glu Asp Ala Gln Arg Arg Val Gln Glu Arg Asp
2877             645                 650                 655
2879 Lys Gln Trp Leu Glu His Val Gln Gln Glu Glu Gln Pro Arg Pro Arg
2880             660                 665                 670
2882 Lys Pro His Glu Glu Asp Arg Leu Lys Arg Glu Asp Ser Val Arg Lys
2883         675                 680                 685
2885 Lys Glu Ala Glu Glu Arg Ala Lys Pro Glu Met Gln Asp Lys Gln Ser
2886     690                 695                 700
2888 Arg Leu Phe His Pro His Gln Glu Pro Ala Lys Leu Ala Thr Gln Ala
2889 705                 710                 715                 720
2891 Pro Trp Ser Thr Thr Glu Lys Gly Pro Leu Thr Ile Ser Ala Gln Glu
2892             725                 730                 735
2894 Ser Val Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu Ser Arg
2895             740                 745                 750
2897 Ser His Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met Val Asp
2898         755                 760                 765
2900 Glu Ser Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly
2901     770                 775                 780
2903 Lys Thr Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile Pro Glu Asn
2904 785                 790                 795                 800
2906 Glu Val Pro Thr Pro Ala Lys Pro Val Thr Asp Leu Thr Ser Ala Pro
2907             805                 810                 815
2909 Ala Pro Lys Leu Ala Leu Arg Glu Thr Pro Ala Pro Leu Pro Val Thr
2910             820                 825                 830
2912 Ser Ser Glu Pro Ser Thr Thr Pro Asn Asn Trp Ala Asp Phe Ser Ser
2913         835                 840                 845
2915 Thr Trp Pro Ser Ser Ser Asn Glu Lys Pro Glu Thr Asp Asn Trp Asp
2916     850                 855                 860
2918 Thr Trp Ala Ala Gln Pro Ser Leu Thr Val Pro Ser Ala Gly Gln Leu
```

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2919 865                   870                 875                 880
2921 Arg Gln Arg Ser Ala Phe Thr Pro Ala Thr Ala Thr Gly Ser Ser Pro
2922               885                 890                 895
2924 Ser Pro Val Leu Gly Gln Gly Glu Lys Val Glu Gly Leu Gln Ala Gln
2925               900                 905                 910
2927 Ala Leu Tyr Pro Trp Arg Ala Lys Lys Asp Asn His Leu Asn Phe Asn
2928          915                 920                 925
2930 Lys Ser Asp Val Ile Thr Val Leu Glu Gln Gln Asp Met Trp Trp Phe
2931      930                 935                 940
2933 Gly Glu Val Gln Gly Gln Lys Gly Trp Phe Pro Lys Ser Tyr Val Lys
2934 945                 950                 955                 960
2936 Leu Ile Ser Gly Pro Val Arg Lys Ser Thr Ser Ile Asp Thr Gly Pro
2937               965                 970                 975
2939 Thr Glu Ser Pro Ala Ser Leu Lys Arg Val Ala Ser Pro Ala Ala Lys
2940               980                 985                 990
2942 Pro Ala Ile Pro Gly Glu Glu Phe Ile Ala Met Tyr Thr Tyr Glu Ser
2943          995                 1000                1005
2945 Ser Glu Gln Gly Asp Leu Thr Phe Gln Gln Gly Asp Val Ile Val Val
2946 1010                1015                1020
2948 Thr Lys Lys Asp Gly Asp Trp Trp Thr Gly Thr Val Gly Asp Lys Ser
E--> 2949 (025)/025           1030                1035                1040
2951 Gly Val Phe Pro Ser Asn Tyr Val Arg Leu Lys Asp Ser Glu Gly Ser
2952               1045                1050                1055
2954 Gly Thr Ala Gly Lys Thr Gly Ser Leu Gly Lys Lys Pro Glu Ile Ala
2955      1060                1065                1070
2957 Gln Val Ile Ala Ser Tyr Ala Ala Thr Gly Pro Glu Gln Leu Thr Leu
2958      1075                1080                1085
2960 Ala Pro Gly Gln Leu Ile Leu Ile Arg Lys Lys Asn Pro Gly Gly Trp
2961      1090                1095                1100
2963 Trp Glu Gly Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Ile Gly Trp
E--> 2964 (105)           1110                1115                1120
2966 Phe Pro Ala Asn Tyr Val Lys Leu Leu Ser Pro Gly Thr Ser Lys Ile
2967               1125                1130                1135
2969 Thr Pro Thr Glu Leu Pro Lys Thr Ala Val Gln Pro Ala Val Cys Gln
2970          1140                1145                1150
2972 Val Ile Gly Met Tyr Asp Tyr Thr Ala Gln Asn Asp Asp Glu Leu Ala
2973      1155                1160                1165
2975 Phe Ser Lys Gly Gln Ile Ile Asn Val Leu Asn Lys Glu Asp Pro Asp
2976    1170                1175                1180
2978 Trp Trp Lys Gly Glu Val Ser Gly Gln Val Gly Leu Phe Pro Ser Asn
E--> 2979 (185)           1190                1195                1200
2981 Tyr Val Lys Leu Thr Thr Asp Met Asp Pro Ser Gln Gln Trp Cys Ser
2982               1205                1210                1215
2984 Asp Leu His Leu Leu Asp Met Leu Thr Pro Thr Glu Arg Lys Arg Gln
2985          1220                1225                1230
2987 Gly Tyr Ile His Glu Leu Ile Val Thr Glu Glu Asn Tyr Val Asn Asp
2988      1235                1240                1245
2990 Leu Gln Leu Val Thr Glu Ile Phe Gln Lys Pro Leu Thr Glu Ser Glu
2991    1250                1255                1260
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      2993 Leu Leu Thr Glu Lys Glu Val Ala Met Ile Phe Val Asn Trp Lys Glu
                               1270                1275                1280
E--> 2994 265 Leu Ile Met Cys Asn Ile Lys Leu Leu Lys Ala Leu Arg Val Arg Lys
      2997           1285                1290                      1295
      2999 Lys Met Ser Gly Glu Lys Met Pro Val Lys Met Ile Gly Asp Ile Leu
      3000           1300                1305                1310
      3002 Ser Ala Gln Leu Pro His Met Gln Pro Tyr Ile Arg Phe Cys Ser Cys
      3003     1315                1320                      1325
      3005 Gln Leu Asn Gly Ala Ala Leu Ile Gln Gln Lys Thr Asp Glu Ala Pro
      3006     1330                      1335                1340
      3008 Asp Phe Lys Glu Phe Val Lys Arg Leu Ala Met Asp Pro Arg Cys Lys
                               1350                1355                1360
E--> 3009 345 Gly Met Pro Leu Ser Ser Phe Ile Leu Lys Pro Met Gln Arg Val Thr
      3012           1365                1370                      1375
      3014 Arg Tyr Pro Leu Ile Ile Lys Asn Ile Leu Glu Asn Thr Pro Glu Asn
      3015           1380                1385                1390
      3017 His Pro Asp His Ser His Leu Lys His Ala Leu Glu Lys Ala Glu Glu
      3018     1395                1400                      1405
      3020 Leu Cys Ser Gln Val Asn Glu Gly Val Arg Glu Lys Glu Asn Ser Asp
      3021     1410                1415                1420
      3023 Arg Leu Glu Trp Ile Gln Ala His Val Gln Cys Glu Gly Leu Ser Glu
                               1430                1435                1440
E--> 3024 425 Gln Leu Val Phe Asn Ser Val Thr Asn Cys Leu Gly Pro Arg Lys Phe
      3027           1445                1450                      1455
      3029 Leu His Ser Gly Lys Leu Tyr Lys Ala Lys Ser Asn Lys Glu Leu Tyr
      3030           1460                1465                1470
      3032 Gly Phe Leu Phe Asn Asp Phe Leu Leu Leu Thr Gln Ile Thr Lys Pro
      3033     1475                1480                      1485
      3035 Leu Gly Ser Ser Gly Thr Asp Lys Val Phe Ser Pro Lys Ser Asn Leu
      3036     1490                1495                1500
      3038 Gln Tyr Lys Met Tyr Lys Thr Pro Ile Phe Leu Asn Glu Val Leu Val
                               1510                1515                1520
E--> 3039 505 Lys Leu Pro Thr Asp Pro Ser Gly Asp Glu Pro Ile Phe His Ile Ser
      3042           1525                1530                      1535
      3044 His Ile Asp Arg Val Tyr Thr Leu Arg Ala Glu Ser Ile Asn Glu Arg
      3045           1540                1545                1550
      3047 Thr Ala Trp Val Gln Lys Ile Lys Ala Ala Ser Glu Leu Tyr Ile Glu
      3048     1555                1560                      1565
      3050 Thr Glu Lys Lys Lys Arg Glu Lys Ala Tyr Leu Val Arg Ser Gln Arg
      3051     1570                1575                1580
      3053 Ala Thr Gly Ile Gly Arg Leu Met Val Asn Val Val Glu Gly Ile Glu
                               1590                1595                1600
E--> 3054 585 Leu Lys Pro Cys Arg Ser His Gly Lys Ser Asn Pro Tyr Cys Glu Val
      3057           1605                1610                      1615
      3059 Thr Met Gly Ser Gln Cys His Ile Thr Lys Thr Ile Gln Asp Thr Leu
      3060           1620                1625                1630
      3062 Asn Pro Lys Trp Asn Ser Asn Cys Gln Phe Phe Ile Arg Asp Leu Glu
      3063     1635                1640                      1645
      3065 Gln Glu Val Leu Cys Ile Thr Val Phe Glu Arg Asp Gln Phe Ser Pro
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3066    1650              1655                 1660
3068 Asp Asp Phe Leu Gly Arg Thr Glu Ile Arg Val Ala Asp Ile Lys Lys
E--> 3069 (665)          1670                 1675              1680
3071 Asp Gln Gly Ser Lys Gly Pro Val Thr Lys Cys Leu Leu Leu His Glu
3072            1685              1690                 1695
3074 Val Pro Thr Gly Glu Ile Val Val Arg Leu Asp Leu Gln Leu Phe Asp
3075            1700              1705                 1710
3077 Glu Pro
3717 <210> SEQ ID NO: 27
3718 <211> LENGTH: 1658
3719 <212> TYPE: PRT
3720 <213> ORGANISM: Mus musculus
3722 <400> SEQUENCE: 27
3723 Met Ala Gln Phe Pro Thr Ala Met Asn Gly Gly Pro Asn Met Trp Ala
3724    1              5                 10                 15
3726 Ile Thr Ser Glu Glu Arg Thr Lys His Asp Lys Gln Phe Asp Asn Leu
3727            20                 25                 30
3729 Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Thr Phe Phe
3730            35                 40                 45
3732 Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu
3733            50                 55                 60
3735 Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile
3736    65                 70                 75                 80
3738 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro Val
3739            85                 90                 95
3741 Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile
3742            100                105                110
3744 Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln
3745            115                120                125
3747 Pro Leu Pro Pro Val Ala Pro Ile Ala Thr Pro Leu Ser Ser Ala Thr
3748            130                135                140
3750 Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro
3751 145                150                155                160
3753 Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln
3754            165                170                175
3756 Pro Leu Ser Ile Pro Tyr Ser Ser Ser Thr Leu Pro His Ala Ser Ser
3757            180                185                190
3759 Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala
3760            195                200                205
3762 Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Ser Ser Ser Ser Thr Ala
3763    210                215                220
3765 Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val
3766 225                230                235                240
3768 Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp
3769            245                250                255
3771 Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu
3772            260                265                270
3774 Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu
3775            275                280                285
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Pgr 14-16

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3777 Ala Asp Ile Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu
3778     290                 295                 300
3780 Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu
3781 305                 310                 315                 320
3783 Thr Leu Pro Pro Glu Leu Val Pro Pro Ser Phe Arg Gly Gly Lys Gln
3784                 325                 330                 335
3786 Val Asp Ser Val Asn Gly Thr Leu Pro Ser Tyr Gln Lys Thr Gln Glu
3787                 340                 345                 350
3789 Glu Glu Pro Gln Lys Lys Leu Pro Val Thr Phe Glu Asp Lys Arg Lys
3790             355                 360                 365
3792 Ala Asn Tyr Glu Arg Gly Asn Met Glu Leu Glu Lys Arg Arg Gln Val
3793     370                 375                 380
3795 Leu Met Glu Gln Gln Gln Arg Glu Ala Glu Arg Lys Ala Gln Lys Glu
3796 385                 390                 395                 400
3798 Lys Glu Glu Trp Glu Arg Lys Gln Arg Glu Leu Gln Glu Gln Glu Trp
3799     .           405                 410                 415
3801 Lys Lys Gln Leu Glu Leu Glu Lys Arg Leu Glu Lys Gln Arg Glu Leu
3802             420                 425                 430
3804 Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg Arg Glu
3805         435                 440                 445
3807 Ala Ala Lys Gln Glu Leu Glu Arg Gln Arg Arg Leu Glu Trp Glu Arg
3808     450                 455                 460
3810 Leu Arg Arg Gln Glu Leu Leu Ser Gln Lys Thr Arg Glu Gln Glu Asp
3811 465                 470                 475                 480
3813 Ile Val Arg Leu Ser Ser Arg Lys Lys Ser Leu His Leu Glu Leu Glu
3814                 485                 490                 495
3816 Ala Val Asn Gly Lys His Gln Gln Ile Ser Gly Arg Leu Gln Asp Val
3817             500                 505                 510
3819 Gln Ile Arg Lys Gln Thr Gln Lys Thr Glu Leu Glu Val Leu Asp Lys
3820         515                 520                 525
3822 Gln Cys Asp Leu Glu Ile Met Glu Ile Lys Gln Leu Gln Gln Glu Leu
3823     530                 535                 540
3825 Lys Glu Tyr Gln Asn Lys Leu Ile Tyr Leu Val Pro Glu Lys Gln Leu
3826 545                 550         :       555                 560
3828 Leu Asn Glu Arg Ile Lys Asn Met Gln Leu Ser Asn Thr Pro Asp Ser
3829             565                 570                 575
3831 Gly Ile Ser Leu Leu His Lys Lys Ser Ser Glu Lys Glu Glu Leu Cys
3832             580                 585                 590
3834 Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser
3835         595                 600                 605
3837 Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Glu Leu Arg
3838     610             .   615                 620       .
3840 Glu Ser Tyr Asn Thr Gln Gln Leu Ala Leu Glu Gln Leu His Lys Ile
3841 625                 630                 635                 640
3843 Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile
3844                 645                 650                 655
3846 Gln Lys Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly
3847             660                 665                 670
3849 Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Glu Lys
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,237

DATE: 01/11/2001
TIME: 17:14:20

Input Set : A:\Egan1.app
Output Set: N:\CRF3\01112001\I674237.raw

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3850            675                  680                  685
3852 Gln Lys Arg Leu Gln Glu Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu
3853      690                  695                  700
3855 Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val
3856 705                  710                  715                  720
3858 Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met
3859                  725                  730                  735
3861 Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly
3862                  740                  745                  750
3864 Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe
3865                  755                  760                  765
3867 Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser
3868      770                  775                  780
3870 Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser
3871 785                  790                  795                  800
3873 Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser
3874                  805                  810                  815
3876 Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe
3877                  820                  825                  830
3879 Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly
3880                  835                  840                  845
3882 Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala
3883      850                  855                  860
3885 Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val
3886 865                  870                  875                  880
3888 Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg
3889                  885                  890                  895
3891 Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val
3892                  900                  905                  910
3894 Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro
3895      915                  920                  925
3897 Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu
3898      930                  935                  940
3900 Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Ser Val Glu Pro Gly Asp Leu
3901 945                  950                  955                  960
3903 Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu
3904                  965                  970                  975
3906 Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn
3907                  980                  985                  990
3909 Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser
3910                  995                  1000                 1005
3912 Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala Tyr
3913      1010                 1015                 1020
3915 Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln Leu Ile
3916 1025                 1030                 1035                 1040
3918 Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly Glu Leu Gln
3919                  1045                 1050                 1055
3921 Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro Ala Ser His Val
3922                  1060                 1065                 1070
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E-->

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     3924 Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met Pro Thr Phe His Ala
     3925        1075               1080                    1085
     3927 Val Cys Gln Val Ile Ala Met Tyr Asp Tyr Met Ala Asn Asn Glu Asp
     3928    1090                   1095                1100
     3930 Glu Leu Asn Phe Ser Lys Gly Gln Leu Ile Asn Val Met Asn Lys Asp
E--> 3931  105                1110          1115                   1120
     3933 Asp Pro Asp Trp Trp Gln Gly Glu Thr Asn Gly Leu Thr Gly Leu Phe
     3934           1125                  1130               1135
     3936 Pro Ser Asn Tyr Val Lys Met Thr Thr Asp Ser Asp Pro Ser Gln Gln
     3937        1140                 1145                      1150
     3939 Trp Cys Ala Asp Leu Gln Ala Leu Asp Thr Met Gln Pro Thr Glu Arg
     3940    1155                 1160                   1165
     3942 Lys Arg Gln Gly Tyr Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr
     3943    1170                 1175                  1180
     3945 Met Asp Asp Asp Leu Gln Leu Val Ile Glu Val Phe Gln Lys Arg Met
E--> 3946  185              1190                 1195                  1200
     3948 Ala Glu Glu Gly Phe Leu Thr Glu Ala Asp Met Ala Leu Ile Phe Val
     3949              1205                1210                   1215
     3951 Asn Trp Lys Glu Leu Ile Met Ser Asn Thr Lys Leu Leu Arg Ala Leu
     3952        1220                 1225                  1230
     3954 Arg Val Arg Lys Lys Thr Gly Gly Glu Lys Met Pro Val Gln Met Ile
     3955    1235                  1240                   1245
     3957 Gly Asp Ile Leu Ala Ala Glu Leu Ser His Met Gln Ala Tyr Ile Arg
     3958    1250                 1255                  1260
     3960 Phe Cys Ser Cys Gln Leu Asn Gly Ala Thr Leu Leu Gln Gln Lys Thr
E--> 3961  265                1270                 1275                  1280
     3963 Asp Glu Asp Thr Asp Phe Lys Glu Phe Leu Lys Lys Leu Ala Ser Asp
     3964              1285                1290                   1295
     3966 Pro Arg Cys Lys Gly Met Pro Leu Ser Ser Phe Leu Leu Lys Pro Met
     3967        1300                 1305                   1310
     3969 Gln Arg Ile Thr Arg Tyr Pro Leu Leu Ile Arg Ser Ile Leu Glu Asn
     3970    1315                 1320                   1325
     3972 Thr Pro Gln Ser His Val Asp His Ser Ser Leu Lys Leu Ala Leu Glu
     3973    1330                 1335                1340
     3975 Arg Ala Glu Glu Leu Cys Ser Gln Val Asn Glu Gly Val Arg Glu Lys
E--> 3976  345              1350                 1355                  1360
     3978 Glu Asn Ser Asp Arg Leu Glu Trp Ile Gln Ala His Val Gln Cys Glu
     3979              1365                1370                   1375
     3981 Gly Leu Ala Glu Gln Leu Ile Phe Asn Ser Leu Thr Asn Cys Leu Gly
     3982        1380                 1385                   1390
     3984 Pro Arg Lys Leu Leu His Ser Gly Lys Leu Tyr Lys Thr Lys Ser Asn
     3985    1395                 1400                1405
     3987 Lys Glu Leu His Ala Phe Leu Phe Asn Asp Phe Leu Leu Leu Thr Tyr
     3988    1410                 1415                 1420
     3990 Leu Val Arg Gln Phe Ala Ala Ala Ser Gly His Glu Lys Leu Phe Asn
E--> 3991  425              1430                 1435                  1440
     3993 Ser Lys Ser Ser Ala Gln Phe Arg Met Tyr Lys Thr Pro Ile Phe Leu
     3994              1445                1450                   1455
     3996 Asn Glu Val Leu Val Lys Leu Pro Thr Asp Pro Ser Gly Asp Glu Pro
```

```
       3997          1460              1465              1470
       3999 Val Phe His Ile Ser His Ile Asp Arg Val Tyr Thr Leu Arg Thr Asp
       4000          1475              1480              1485
       4002 Asn Ile Asn Glu Arg Thr Ala Trp Val Gln Lys Ile Lys Gly Ala Ser
       4003     1490              1495              1500
       4005 Glu Gln Tyr Ile Asp Thr Glu Lys Lys Lys Arg Glu Lys Ala Tyr Gln
E--> 4006 (505)           1510              1515              1520
       4008 Ala Arg Ser Gln Lys Thr Ser Gly Ile Gly Arg Leu Met Val His Val
       4009          1525              1530              1535
       4011 Ile Glu Ala Thr Glu Leu Lys Ala Cys Lys Pro Asn Gly Lys Ser Asn
       4012          1540              1545              1550
       4014 Pro Tyr Cys Glu Val Ser Met Gly Ser Gln Ser Tyr Thr Thr Arg Thr
       4015     1555              1560              1565
       4017 Leu Gln Asp Thr Leu Asn Pro Lys Trp Asn Phe Asn Cys Gln Phe Phe
       4018     1570              1575              1580
       4020 Ile Lys Asp Leu Tyr Gln Asp Val Leu Cys Leu Thr Met Phe Asp Arg
E--> 4021 (585)           1590              1595              1600
       4023 Asp Gln Phe Ser Pro Asp Asp Phe Leu Gly Arg Thr Glu Val Pro Val
       4024          1605              1610              1615
       4026 Ala Lys Ile Arg Thr Glu Gln Glu Ser Lys Gly Pro Thr Thr Arg Arg
       4027          1620              1625              1630
       4029 Leu Leu Leu His Glu Val Pro Thr Gly Glu Val Trp Val Arg Phe Asp
       4030     1635              1640              1645
       4032 Leu Gln Leu Phe Glu Gln Lys Thr Leu Leu
       4033     1650              1655
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see following page for more errors

<210> 18

<211> 1521

<212> DNA

<213> Mus musculus

<400> 18

gagaaggcgg cctgccgcag cgggacaacc tagagcgcga cgtggaggcg cgtagcggag 60

ctggagcaac tgcgcaccga ggtggatgtg cgcattagcg cnntggacac ctgcgtcaag 120 → see item 10 on Error Summary Sheet

gccaagtcgc tgccagccgt cccgccgaga gtctcaggcc cacccccgaa ccctccaccc 180

attgatccag ctagcctgga ggaattcaag aaaaggatcc tggagtctca gcggctccct 240

gtagtcaacc ctgcwgccca acccagcggt tgagraccca gctgccgcag gacgctgggt 300

gccagaatcg cccacctgtg gatgggggca gccaggtgcc cacagtgctg gacacccgcc 360

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agctgccacc ctaggcaact cctccggttt cctatcactc tgctcctgac ccgggaggtg 600

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only errored portion of Sequence 18 shown

Input Set : A:\Egan1.app
Output Set: N:\CRF3\01112001\I674237.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:711 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
M:332 Repeated in SeqNo=3
L:1421 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
M:332 Repeated in SeqNo=6
L:1979 M:258 W: Mandatory Feature missing, .220> not found for SEQ ID#:18
L:1979 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:1979 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:1979 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18
L:1979 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:2747 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:2949 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24
M:332 Repeated in SeqNo=24
L:3916 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
M:332 Repeated in SeqNo=27